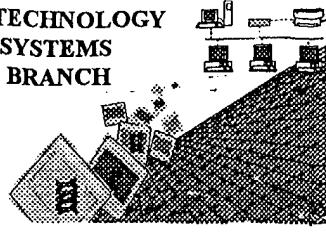# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US/10/651,584

Source: _IFWO_

Date Processed by STIC: 12/10/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/651,584_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                        prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                        ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                        each n or Xaa can only represent a single residue. Please present the maximum number of each
                        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                        previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                        the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                        Artificial or Unknown sequences.

7____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                        (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                        (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                        This sequence is intentionally skipped

                        Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
                        <400> sequence id number
                        000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                        In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                        is Artificial Sequence

11____Use of <220>   Sequence(s) _1-20_ missing the <220> "Feature" and associated numeric identifiers and responses.
                        Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                        "Unknown." Please explain source of genetic material in <220> to <223> section.
                        (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                        listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 12/10/2003
PATENT APPLICATION: **US/10/651,584** TIME: 17:24:47

  Input Set : **A:\PTO.YF.asc**
  Output Set: **N:\CRF4\12102003\J651584.raw**

W-->   1 35
   3 <110> APPLICANT: Lauermann, Vit
   5 <120> TITLE OF INVENTION: Targeted release
W-->   7 <130> **FILE REFERENCE:**
C-->   9 <140> **CURRENT APPLICATION NUMBER: US/10/651,584**
   11 <141> CURRENT FILING DATE: 2003-08-30
   13 <160> NUMBER OF SEQ ID NOS: 111

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

   17 <210> SEQ ID NO: 1
   19 <211> LENGTH: 7
E--> 21 <212> TYPE: peptide
   23 <213> ORGANISM: unknown
W--> 26 <220> FEATURE:
W--> 26 <223> OTHER INFORMATION:
W--> 26 <400> 1
   28 SMSIARL
   32 <210> SEQ ID NO: 2
   34 <211> LENGTH: 13
E--> 36 <212> TYPE: peptide
   38 <213> ORGANISM: unknown
W--> 41 <220> FEATURE:
W--> 41 <223> OTHER INFORMATION:
W--> 41 <400> 2
   43 SKGSFSIQYT YHV
   47 <210> SEQ ID NO: 3
   49 <211> LENGTH: 13
E--> 51 <212> TYPE: peptide
   53 <213> ORGANISM: unknown
W--> 56 <220> FEATURE:
W--> 56 <223> OTHER INFORMATION:
W--> 56 <400> 3
   58 HLGGSQQLLH NKQ
   62 <210> SEQ ID NO: 4
   64 <211> LENGTH: 14
E--> 66 <212> TYPE: peptide
   68 <213> ORGANISM: unknown
W--> 71 <220> FEATURE:
W--> 71 <223> OTHER INFORMATION:
W--> 71 <400> 4
   73 SKGKGTSSQY SNTE

[Handwritten annotations:]
- Use Prt, For a protein sequence.
- Incomplete response, please see item 11, on error summary sheet. (P. 1-4)
- One letter Amino Acid designations are not to be used in a sequence. Please use 3 letter Amino Acids.
- Same error
- Same error
- 13 Please see Attached sample sequence listing format.
- FYI: Number the amino Acids under every five Amino Acids, do not use tab codes.

RAW SEQUENCE LISTING   DATE: 12/10/2003
PATENT APPLICATION: US/10/651,584   TIME: 17:24:47

Input Set : A:\PTO.YF.asc
Output Set: N:\CRF4\12102003\J651584.raw

```
        77 <210> SEQ ID NO: 5
        79 <211> LENGTH: 8
E-->    81 <212> TYPE: peptide           SAme error
        83 <213> ORGANISM: unknown
W-->    86 <220> FEATURE:
W-->    86 <223> OTHER INFORMATION:
W-->    86 <400> 5
        88 DRVYIHPF                                            8
        92 <210> SEQ ID NO: 6
        94 <211> LENGTH: 12
E-->    96 <212> TYPE: peptide           SAme error
        98 <213> ORGANISM: unknown
W-->   101 <220> FEATURE:
W-->   101 <223> OTHER INFORMATION:
W-->   101 <400> 6
       103 VVCGERGFFY TP                                      12
       107 <210> SEQ ID NO: 7
       109 <211> LENGTH: 7
E-->   111 <212> TYPE: peptide           SAme error
       113 <213> ORGANISM: unknown
W-->   116 <220> FEATURE:
W-->   116 <223> OTHER INFORMATION:
W-->   116 <400> 7
       118 FFYTPKA                                             7
       122 <210> SEQ ID NO: 8
       124 <211> LENGTH: 9
E-->   126 <212> TYPE: peptide           SAme error
       128 <213> ORGANISM: unknown
W-->   131 <220> FEATURE:
W-->   131 <223> OTHER INFORMATION:
W-->   131 <400> 8
       133 KRRPVKVYP                                           9
       137 <210> SEQ ID NO: 9
       139 <211> LENGTH: 12
E-->   141 <212> TYPE: peptide
       143 <213> ORGANISM: unknown
W-->   146 <220> FEATURE:               SAme error
W-->   146 <223> OTHER INFORMATION:
W-->   146 <400> 9
       148 PVGKKRRPVK VY                                      12
       152 <210> SEQ ID NO: 10
       154 <211> LENGTH: 12
E-->   156 <212> TYPE: peptide
       158 <213> ORGANISM: unknown
W-->   162 <220> FEATURE:               SAme error
W-->   162 <223> OTHER INFORMATION:
W-->   162 <400> 10
       166 KPVGKKRRPV KV                                      12
       168 <210> SEQ ID NO: 11
```

RAW SEQUENCE LISTING   DATE: 12/10/2003
PATENT APPLICATION: US/10/651,584   TIME: 17:24:47

Input Set : A:\PTO.YF.asc
Output Set: N:\CRF4\12102003\J651584.raw

```
         170 <211> LENGTH: 12
E--> 172 <212> TYPE: peptide
         174 <213> ORGANISM: unknown
W--> 177 <220> FEATURE:                    same error
W--> 177 <223> OTHER INFORMATION:
W--> 177 <400> 11
         179 GKPVGKKRRP VK                                  12
         183 <210> SEQ ID NO: 12
         185 <211> LENGTH: 13
E--> 187 <212> TYPE: peptide               same error
         189 <213> ORGANISM: unknown
W--> 192 <220> FEATURE:
W--> 192 <223> OTHER INFORMATION:
W--> 192 <400> 12
         194 TFAGNAVRRS VGQ                                 13
         198 <210> SEQ ID NO: 13
         200 <211> LENGTH: 6
E--> 202 <212> TYPE: peptide               same error
         204 <213> ORGANISM: unknown
W--> 207 <220> FEATURE:
W--> 207 <223> OTHER INFORMATION:
W--> 207 <400> 13
         209 PLGLWA                                         6
         213 <210> SEQ ID NO: 14
         215 <211> LENGTH: 5
E--> 217 <212> TYPE: peptide               same error
         219 <213> ORGANISM: unknown
W--> 222 <220> FEATURE:
W--> 222 <223> OTHER INFORMATION:
W--> 222 <400> 14
         224 PLFYS                                          5
         228 <210> SEQ ID NO: 15
         230 <211> LENGTH: 5
E--> 232 <212> TYPE: peptide               same error
         234 <213> ORGANISM: unknown
W--> 237 <220> FEATURE:
W--> 237 <223> OTHER INFORMATION:
W--> 237 <400> 15
         239 PRTLT                                          5
         243 <210> SEQ ID NO: 16
         245 <211> LENGTH: 5
E--> 247 <212> TYPE: peptide               same error
         249 <213> ORGANISM: unknown
W--> 252 <220> FEATURE:
W--> 252 <223> OTHER INFORMATION:
W--> 252 <400> 16
         254 PLRLS                                          5
         258 <210> SEQ ID NO: 17
         260 <211> LENGTH: 6
```

RAW SEQUENCE LISTING   DATE: 12/10/2003
PATENT APPLICATION: **US/10/651,584**   TIME: 17:24:47

Input Set : **A:\PTO.YF.asc**
Output Set: **N:\CRF4\12102003\J651584.raw**

```
E--> 262 <212> TYPE: peptide
     264 <213> ORGANISM: unknown          SAme error
W--> 267 <220> FEATURE:
W--> 267 <223> OTHER INFORMATION:
W--> 267 <400> 17
     269 HSSKLQ                                              6
     273 <210> SEQ ID NO: 18
     275 <211> LENGTH: 6
E--> 277 <212> TYPE: peptide
     279 <213> ORGANISM: unknown          SAme error
W--> 282 <220> FEATURE:
W--> 282 <223> OTHER INFORMATION:
W--> 282 <400> 18
     284 SQYSNT                                              6
     288 <210> SEQ ID NO: 19
     290 <211> LENGTH: 7
E--> 292 <212> TYPE: peptide
     294 <213> ORGANISM: unknown          SAme error
W--> 297 <220> FEATURE:
W--> 297 <223> OTHER INFORMATION:
W--> 297 <400> 19
     299 QFYSSNK                                             7
     303 <210> SEQ ID NO: 20
     305 <211> LENGTH: 12
E--> 307 <212> TYPE: peptide
     309 <213> ORGANISM: unknown          SAme error
W--> 312 <220> FEATURE:
W--> 312 <223> OTHER INFORMATION:
W--> 312 <400> 20
     314 VSQNYPIVQN FN                                       12
```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/10/2003
PATENT APPLICATION: US/10/651,584   TIME: 17:24:48

Input Set : **A:\PTO.YF.asc**
Output Set: **N:\CRF4\12102003\J651584.raw**

Error explanation

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51
Seq#:52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75
Seq#:76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99
Seq#:100,101,102,103,104,105,106,107,108,109,110,111

VERIFICATION SUMMARY　　　　　　　　DATE: 12/10/2003
PATENT APPLICATION:　**US/10/651,584**　　　TIME: 17:24:48

Input Set : **A:\PTO.YF.asc**
Output Set: **N:\CRF4\12102003\J651584.raw**

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:7 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:unknown
L:26 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:unknown
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26
L:36 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:41 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:41
L:51 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:56 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:unknown
L:56 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:unknown
L:56 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56
L:66 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:unknown
L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:unknown
L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71
L:81 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:unknown
L:86 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:unknown
L:86 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:86
L:96 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:unknown
L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:unknown
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:101
L:111 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:unknown
L:116 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:unknown
L:116 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:116
L:126 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:131 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:unknown
L:131 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:unknown
L:131 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:131
L:141 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:146 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>

```
ORGANISM:unknown
L:146 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:unknown
L:146 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:146
L:156 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:unknown
L:162 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:unknown
L:162 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:162
L:172 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:unknown
L:177 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:unknown
L:177 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:177
L:187 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
```

VERIFICATION SUMMARY   DATE: 12/10/2003
PATENT APPLICATION: **US/10/651,584**   TIME: 17:24:48

Input Set : **A:\PTO.YF.asc**
Output Set: **N:\CRF4\12102003\J651584.raw**

L:192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:unknown
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:unknown
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:192
L:202 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:207 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:unknown
L:207 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:unknown
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:207
L:217 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:222 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:unknown
L:222 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:unknown
L:222 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:222
L:232 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:unknown
L:237 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:unknown
L:237 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:237
L:247 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:unknown
L:252 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:unknown
L:252 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:252
L:262 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:unknown
L:267 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:unknown
L:277 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:292 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:307 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:322 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:337 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:352 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:367 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:382 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:397 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:412 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:427 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:442 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:457 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:472 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:487 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:502 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:517 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:532 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:547 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

```
L:563 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:578 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:593 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:608 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:623 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:638 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:653 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:668 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
```

VERIFICATION SUMMARY   DATE: 12/10/2003
PATENT APPLICATION: **US/10/651,584**   TIME: 17:24:48

Input Set : **A:\PTO.YF.asc**
Output Set: **N:\CRF4\12102003\J651584.raw**

```
L:683 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:698 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:713 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:728 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:743 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:758 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
```

<110>   Smith, John; Smithgene Inc.

<120>   Example of a Sequence Listing

<130>   01-00001

<140>   PCT/EP98/00001
<141>   1998-12-31

<150>   US 08/999,999
<151>   1997-10-15

<160>   <

<170>   PatentIn version 2.0

<210>   1
<211>   389
<212>   DNA
<213>   Paramecium sp.

<220>
<221>   CDS
<222>   (279)...(389)

<300>
<301>   Doe, Richard
<302>   Isolation and Characterization of a Gene Encoding a
          Protease from Paramecium sp.
<303>   Journal of Genes
<304>   1
<305>   4
<306>   1-7
<307>   1988-06-31
<308>   123456
<309>   1988-06-31

<400>   1
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agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggcd ggcaggcagc   120

tgatgtggca attgctggca gtgccacagg cctttcagcc aggcttaggg tgggttccgc   180

cgcggcgcgg cggcccctct cgcgctcctc tcgcgcctct ctctcgctct cctctcgctc   240

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ggacctgatt  aggtgagcag  gaggaggggg  cagttagc        atg  gtt  tca  atg  ttc  agc   296
                                                     Met  Val  Ser  Met  Phe  Ser
                                                     1                    5

ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  gtt  gtt  tgt  ttg  ttc  caa   344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
              10                         15                        20

tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt        389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
              25                         30                        35
```

<210>   2
<211>   37
<212>   PRT
<213>   Paramecium sp.

<400>   2

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Met  Val  Ser  Met  Phe  Ser  Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu
1                   5                        10                        15

Phe  Val  Cys  Leu  Phe  Gln  Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser
              20                        25                        30

Leu  Gln  Pro  Asn  Leu
              35
```

<210>   3
<211>   11
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Designed peptide based on size and polarity to act as a
         linker between the alpha and beta chains of Protein XYZ.

<400>   3

```
Met  Val  Asn  Leu  Glu  Pro  Met  His  Thr  Glu  Ile
1                   5                        10
```

<210>   4
<400>   4
000

[Annex VIII follows]

Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

		cule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

<223>	Other Infor-mation	Other relevant information; four lines maximum	M, under the fol-lowing conditions: if "n," "Xaa," or a modified or un-usual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is com-bined DNA/RNA
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publi-cation; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MM-yyyy or Season-yyyy	O
<300>	Database Accession Number	Accession number assigned by data-base including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

		type citations only; specify as yyyy-mm-dd	
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by   1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer-readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;